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<!--StartFragment-->RESULT 2
ADX61938
ID   ADX61938 standard; cDNA; 2124 BP.
XX
AC   ADX61938;
XX
DT   21-APR-2005 (first entry)
XX
DE   Plant full length insert polynucleotide seqid 32781.
XX
KW   plant protectant; plant growth regulant; gene therapy; plant;
KW   recombinant DNA construct; physical array; plant breeding marker;
KW   cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW   extreme osmotic condition; pathogen tolerance; pest tolerance;
KW   growth rate; cell cycle pathway; disease resistance;
KW   galactomannan production; lignin production; plant growth regulator;
KW   yield; plant growth; plant development; seed oil; protein yield;
KW   protein content; gene; ss.
XX
OS   Unidentified.
XX
PN   US2004034888-A1.
XX
PD   19-FEB-2004.
XX
PF   28-APR-2003; 2003US-00425114.
XX
PR   06-MAY-1999; 99US-00304517.
PR   05-NOV-2001; 2001US-00985678.
XX
PA   (LIUJ/) LIU J.
PA   (ZHOU/) ZHOU Y.
PA   (KOVA/) KOVALIC D K.
PA   (SCRE/) SCREEN S E.
PA   (TABA/) TABASKA J E.
PA   (CAOY/) CAO Y.
XX
PI   Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
DR   WPI; 2004-180133/17.
XX
PT   New recombinant DNA construct, useful for improving plant tolerance to
PT   cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT   pests, for conferring increased resistance to plant disease, or for
PT   improving yield.
XX
PS   Claim 1; SEQ ID NO 32781; 15pp; English.
XX
CC   The invention describes a recombinant DNA construct comprising a
CC   polynucleotide consisting of a sequence encoding an amino acid sequence
CC   available in electronic form from the US patent office at
CC   ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC   of the invention are also useful in physical arrays of molecules and as
CC   plant breeding markers. The recombinant DNA construct is useful for
CC   improving plant tolerance to cold, heat, drought, herbicides, extreme
CC   osmotic conditions, pathogens or pests, for manipulating growth rate in
CC   plant cells by modification of the cell cycle pathway, for conferring
CC   increased resistance to plant disease, for producing galactomannan,
CC   lignin or plant growth regulators, for increasing the rate of homologous
CC   recombination in plants, for improving yield by modification of
CC   photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

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CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.

XX

SQ Sequence 2124 BP; 599 A; 492 C; 463 G; 570 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.55e-201	Length:	2124
Score:	2276.50	Matches:	423
Percent Similarity:	87.6%	Conservative:	63
Best Local Similarity:	76.2%	Mismatches:	52
Query Match:	64.1%	Indels:	17
DB:	13	Gaps:	4

US-10-544-180A-2 (1-673) x ADX61938 (1-2124)

Qy	126	ProAspValLysSerAsnAsnLeuAsnGluLysArgAspSerIleSerLysAspSerIle	145
		::: :::	
Db	263	CCCAACTTTGACCTGCAGAAATGCTCATCGGGTCGA-----AAGGATGGCCCT	310
Qy	146	His-----GlnLysValGluThrProThrLysIleHisArgArgGlnLeuArg	161
		::: ::	
Db	311	CATCTCCTGGGTAGATCAAAGGAAATAACACACATGAAATTAAGGAGAGTTGCTGTAAGG	370
Qy	162	GluLysArgArgGluMetArgAlaAsnGluLeuValGlnHisAsnAspAspThrIleLeu	181
		::: ::: :: ::: :::::	
Db	371	AAGAAAATG-----GAAGTAGTGACGAGGATGATGAAGCGTTAGTT	412
Qy	182	LysLeuGluAsnAlaAlaIleGluArgSerLysSerValAspSerAlaValLeuGlyLys	201
		:::	
Db	413	AAACTTGAGAATGCAGGTATCGAACGTTCAAAGCTGTTGACTCTGCTGTGCTGGGAAAA	472
Qy	202	TyrSerIleTrpArgArgGluAsnGluAsnAspAsnSerAspSerAsnIleArgLeuMet	221
		::: :: ::	
Db	473	TACAGCATCTGGAGACGTGAAATGAAATGAAAAGGCAGATTCAAGGGTCCGTTTGATG	532
Qy	222	ArgAspGlnValIleMetAlaArgValTyrSerGlyIleAlaLysLeuLysAsnLysAsn	241
		::: ::: :: :::::	
Db	533	CGAGATCAAATGATCATGGCCAGAATATATTCTGTTCTTGCCAAATCGAGGGACAAGCTT	592
Qy	242	AspLeuLeuGlnGluLeuGlnAlaArgLeuLysAspSerGlnArgValLeuGlyGluAla	261
		:::	
Db	593	GATCTCTATCAGGAGCTGCTTGCAAGGCTCAAGGAAAGCCAGCGATCCCTTGGGGAAGCT	652
Qy	262	ThrSerAspAlaAspLeuProArgSerAlaHisGluLysLeuArgAlaMetGlyGlnVal	281
		::: ::: ::: ::::: ::	
Db	653	ACTGCTGATGCTGAACCTCCCAAGAGTGCTTCGGATAGAACCAAGCAATGGGCCAAGTT	712
Qy	282	LeuAlaLysAlaLysMetGlnLeuTyrAspCysLysLeuValThrGlyLysLeuArgAla	301
		::: ::: ::: :: ::	
Db	713	TTATCAAAGCAAGGGATCTATTGTACGATTGCAAGGAAATTACCCAGCGTTTGAGAGCA	772
Qy	302	MetLeuGlnThrAlaAspGluGlnValArgSerLeuLysLysGlnSerThrPheLeuAla	321
		::: ::: :: ::	
Db	773	ATGCTTCAGTCAGCAGATGAGCAGGTCCGGAGCTTGAAGAAGCAGAGCACCTTCCTTAGC	832
Qy	322	GlnLeuAlaAlaLysThrIleProAsnProIleHisCysLeuSerMetArgLeuThrIle	341
Db	833	CAGCTAGCAGCTAAGACAATCCCAAATGGCATCCATTGTCTTTCCATGCGCTTAACGATT	892

Qy	342	AspTyrTyrLeuLeuSerProGluLysArgLysPheProArgSerGluAsnLeuGluAsn	361
Db	893		952
Qy	362	ProAsnLeuTyrHisTyrAlaLeuPheSerAspAsnValLeuAlaAlaSerValValVal	381
Db	953	::	1012
Qy	382	AsnSerThrIleMetAsnAlaLysAspProSerLysHisValPheHisLeuValThrAsp	401
Db	1013		1072
Qy	402	LysLeuAsnPheGlyAlaMetAsnMetTrpPheLeuLeuAsnProProGlyLysAlaThr	421
Db	1073		1132
Qy	422	IleHisValGluAsnValAspGluPheLysTrpLeuAsnSerSerTyrCysProValLeu	441
Db	1133		1192
Qy	442	ArgGlnLeuGluSerAlaAlaMetArgGluTyrTyrPheLysAlaAspHisPro-----	459
Db	1193	::	1252
Qy	460	---ThrSerGlySerSerAsnLeuLysTyrArgAsnProLysTyrLeuSerMetLeuAsn	478
Db	1253	::::	1312
Qy	479	HisLeuArgPheTyrLeuProGluValTyrProLysLeuAsnLysIleLeuPheLeuAsp	498
Db	1313		1372
Qy	499	AspAspIleIleValGlnLysAspLeuThrProLeuTrpGluValAsnLeuAsnGlyLys	518
Db	1373		1432
Qy	519	ValAsnGlyAlaValGluThrCysGlyGluSerPheHisArgPheAspLysTyrLeuAsn	538
Db	1433		1492
Qy	539	PheSerAsnProHisIleAlaArgAsnPheAsnProAsnAlaCysGlyTrpAlaTyrGly	558
Db	1493		1552
Qy	559	MetAsnMetPheAspLeuLysGluTrpLysLysArgAspIleThrGlyIleTyrHisLys	578
Db	1553		1612
Qy	579	TrpGlnAsnMetAsnGluAsnArgThrLeuTrpLysLeuGlyThrLeuProProGlyLeu	598
Db	1613		1672
Qy	599	IleThrPheTyrGlyLeuThrHisProLeuAsnLysAlaTrpHisValLeuGlyLeuGly	618
Db	1673	::	1732
Qy	619	TyrAsnProSerIleAspLysLysAspIleGluAsnAlaAlaValValHisTyrAsnGly	638
Db	1733		1792

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Qy      639 AsnMetLysProTrpLeuGluLeuAlaMetSerLysTyrArgProTyrTrpThrLysTyr 658
          |||||::|
Db      1793 AACATGAAGCCCTGGCTGGAAATTGCAATGATAAAGTATCGGCCTTACTGGACAAAGTAC 1852

Qy      659 IleLysPheAspHisProTyrLeuArgArgCysAsnLeuHisGlu 673
          |||::| |||::| |||::|
Db      1853 ATCAATTATCAGCATTCTTACATTCATGGATGCAAGATCAGCAA 1897
    
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<!--EndFragment-->